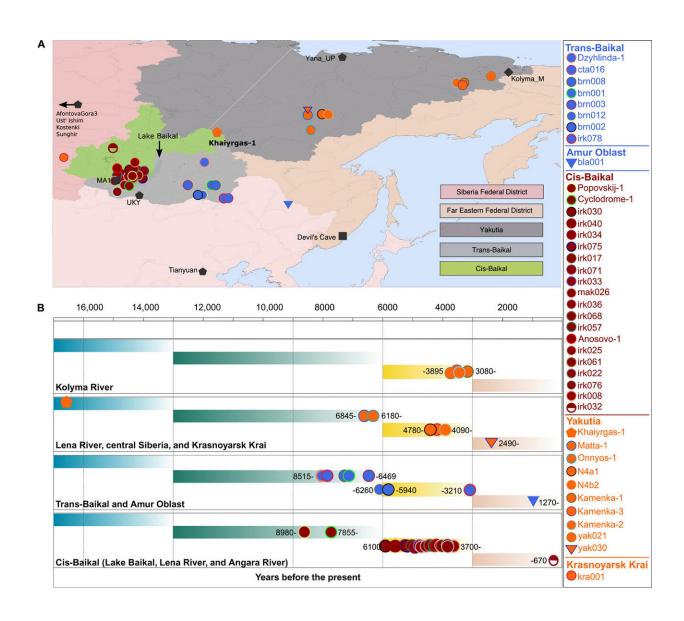


Genome study of people living Asia from Stone Age through Medieval period

January 7 2021, by Bob Yirka



Geographical and chronological information concerning the ancient individuals. (A) Geographical map showing the locations of the individuals sequenced in this



study (orange, blue, and red). Genomes published elsewhere are shown as black (see table S2 for information about all published individuals used in comparative analysis). (B) Timeline showing the ages of the ancient individuals as calibrated years before the present. Credit: *Science Advances* (2021). DOI: 10.1126/sciadv.abc4587

An international team of researchers has conducted a genomic study of 40 human remains recovered from parts of upper east Asia in what is now mostly Siberia. In their paper published in the journal *Science Advances*, the group describes their study and what it demonstrated about population shifts and migration in the region.

Modern upper east Asia includes parts of Russia and Mongolia, and because of its cold weather, is very sparsely populated. Prior research has shown that despite the frigid temperatures, people have been living in upper east Asia for thousands of years. In this new effort, the researchers conducted an extensive genomic study of the remains of 40 people who have been excavated across the region over many years. The remains ranged from 16,900 to 550 years old (from the stone age through the medieval period) and were mostly from the Trans-Baikal Yakutia, Cis-Baikal, Amur Oblast and Krasnoyarsk Krai regions. The work involved sequencing the genomes of all 40 of the people under study and then using the data to learn more about them.

In studying the genes of the people that lived in the region over time (and creating statistical models), the researchers were able to spot changes in population in different areas and to follow groups as they moved around. In so doing, they found that the Belkachi people, originally from Yakutia, were the ancestors of people who later lived in the Saqqaq Arctic. They also found that the <u>oldest person</u> studied was a 17,000-year-old female from a dig site in Khaiyrgas Cave who



represented the first known human inhabitants of the region after the last great Ice Age.

The researchers also found evidence of the bacterium that causes plague in two of the people and that the ages of those individuals coincided with a drop in genetic diversity in the region, which suggested a drop in population. And when they compared the genes of those under study with genetic data obtained through other studies, they found that people from the Lake Baikal area, and also from some areas farther east, interbred with people both inside and outside of Siberia from the latter parts of the stone age right up to medieval times.

More information: Gülşah Merve Kılınç et al. Human population dynamics and Yersinia pestis in ancient northeast Asia, *Science Advances* (2021). DOI: 10.1126/sciadv.abc4587

Press release

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